

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.
- 10 (ii) TITLE OF INVENTION: Apo-2 Receptor
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
20 (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
- 25 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- 35 (A) NAME: Marschang, Diane L.  
(B) REGISTRATION NUMBER: 35,600  
(C) REFERENCE/DOCKET NUMBER: P1101R2

## (ix) TELECOMMUNICATION INFORMATION:

- 40 (A) TELEPHONE: 650/225-5416  
(B) TELEFAX: 650/952-9881

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 411 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro  
20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp  
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser  
65 70 75

	Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Glu	Asp	
						80				85				90	
5	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
					95					100					105
	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
					110					115					120
10	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
					125					130					135
	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
					140					145					150
15	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
					155					160					165
20	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
					170					175					180
	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
					185					190					195
25	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys
					200					205					210
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp
					215					220					225
30	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp
					230					235					240
35	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val
					245					250					255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly
					260					265					270
40	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro
					275					280					285
	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala
					290					295					300
45	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp
					305					310					315
	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg
50					320					325					330
	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu
					335					340					345
55	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp
					350					355					360
	Val	Asn	Lys	Thr	Gly	Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp
					365					370					375
60	Ala	Leu	Glu	Thr	Leu	Gly	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu
					380					385					390
	Asp	His	Leu	Leu	Ser	Ser	Gly	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn

Ala Asp Ser Ala Xaa Ser  
410 411

5

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

20

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
Met Glu  
1

25

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
5 10 15

30

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala  
20 25

35

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
45 50

40

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
55 60 65

45

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
70 75 80

50

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
85 90

55

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457  
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His  
95 100 105

60

TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496  
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys  
110 115

GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535  
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr  
120 125 130

10052798-110304

AGA AAC ACA GTG GT CAG TGC GAA GAA GGC ACC TTC 574  
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg  
 135 140 145

5 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613  
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr  
 150 155

10 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652  
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr  
 160 165 170

15 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691  
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly  
 175 180

20 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730  
 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile  
 185 190 195

25 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769  
 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys  
 200 205 210

30 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808  
 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly  
 215 220

35 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847  
 Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro  
 225 230 235

40 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886  
 Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile  
 240 245

45 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925  
 Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val  
 250 255 260

50 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964  
 Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser  
 265 270 275

55 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003  
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala  
 280 285

60 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042  
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn  
 290 295 300

GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081  
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp  
 305 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120  
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro  
 315 320 325

60 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159  
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys  
 330 335 340

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GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TGG 1198  
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
345 350

5 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
355 360 365

10 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
370 375

15 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
380 385 390

20 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
Ala Asp Ser Ala Xaa Ser  
410 411

25 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

30 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTTACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTGGTT TGGGATGTCA 1650

35 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

40 GCGGCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 70 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 29 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:



10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

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20      (1) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 930 base pairs
          (B) TYPE: Nucleic Acid
          (C) STRANDEDNESS: Single
          (D) TOPOLOGY: Linear

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30           ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe

1                          5                         10

[illegible]

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
Pro-Leu-Val-Val-Pro-Phe-Tyr-Ala-Ala-Gln-Pro-Ala-Met  
30 35

40           GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA 153  
Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu

40                         45                         50

45      CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192  
Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser

55                          60

50      GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231  
     Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg  
          65                          70                          75

CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile  
55 80 85 90

AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309  
Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val  
95 100

AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348  
 Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 105 110 115

11032798 110201

TCC CTG TAT CTG AATG AAC AGC CTG AGA GCC GAG 387  
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 120 125

5 ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA 426  
 Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly  
 130 135 140

10 CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG 465  
 Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr  
 145 150 155

15 GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT 504  
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly  
 160 165

20 GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC 543  
 Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp  
 170 175 180

CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC 582  
 Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile  
 185 190

25 ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC 621  
 Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser  
 195 200 205

30 TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC 660  
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val  
 210 215 220

35 ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC 699  
 Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp  
 225 230

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738  
 Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu  
 235 240 245

40 ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777  
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr  
 250 255

45 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816  
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val  
 260 265 270

50 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855  
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala  
 275 280 285

55 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894  
 Ala His His His His His His Gly Ala Ala Glu Gln Lys  
 290 295

CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930  
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 300 305 309

60

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
 10 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
 15 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met  
 30 35

GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153  
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val  
 40 45 50

CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192  
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60

GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231  
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg  
 65 70 75

CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile  
 80 85 90

AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309  
 Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val  
 95 100

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 105 110 115

TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387  
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 120 125

ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426  
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val  
 130 135 140

AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465  
 Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg  
 145 150 155

GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504  
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser  
 160 165

GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu  
 170 175 180

ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582



Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln  
185 190

5 GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621  
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr  
195 200 205

10 TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660  
Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
210 215 220

15 GTA CTT GTC ATC TAT GGT AAA AAC AAC CCG CCC TCA GGG 699  
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly  
225 230

20 ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738  
Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr  
235 240 245

25 GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777  
Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu  
250 255

30 GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816  
Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn  
260 265 270

35 CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855  
His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
275 280 285

40 GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894  
Gly Ala Ala Ala His His His His His His Gly Ala Ala  
290 295

45 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933  
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala  
300 305 310

40 GCA TAG 939  
Ala  
312

(2) INFORMATION FOR SEQ ID NO:8:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 933 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
1 5 10

60 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met

5 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153  
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val  
 40 45 50

10 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192  
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60

15 GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231  
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg  
 65 70 75

20 CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile  
 80 85 90

25 TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309  
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val  
 95 100

30 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC 348  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 105 110 115

35 ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC 387  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 120 125

40 ACG GCT GTG TAT TAC TGT GCG AGA GAT AGG GGC TAC TAC 426  
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Tyr  
 130 135 140

45 TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC 465  
 Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val  
 145 150 155

50 TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504  
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 160 165

55 GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543  
 Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser  
 170 175 180

60 GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582  
 Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys  
 185 190

65 ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621  
 Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val  
 195 200 205

70 CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660  
 His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
 210 215 220

75 CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699  
 Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro  
 225 230

80 GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738  
 Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser

245

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TAG 933

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 309 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
35 1 5 10 15

~~Phe-Asn-Val-Lys-Lys-Leu Leu Phe Ala Ile Pro Leu Val Val Pro~~

20                      25                      30

[illegible]

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser  
50 55 60

45 Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp  
65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile  
50 80 85 90

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly  
95 100 105

55 Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
125 130 135

60 Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp  
140 145 150

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser

55

160

165

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln  
 170 175 180  
 5 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr  
 185 190 195  
 10 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln  
 200 205 210  
 Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn  
 215 220 225  
 15 Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser  
 230 235 240  
 Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp  
 245 250 255  
 20 Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His  
 260 265 270  
 25 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala  
 275 280 285  
 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile  
 290 295 300  
 30 Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 305 309

## (2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15  
 45 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30  
 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu  
 35 40 45  
 50 Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser  
 50 55 60  
 55 Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp  
 65 70 75  
 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile  
 80 85 90  
 60 Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly  
 95 100 105  
 Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 125 130 135  
 5 Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe  
 140 145 150  
 Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly  
 155 160 165  
 10 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu  
 170 175 180  
 Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val  
 185 190 195  
 15 Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser  
 200 205 210  
 20 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 215 220 225  
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly  
 230 235 240  
 25 Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln  
 245 250 255  
 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser  
 260 265 270  
 30 Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
 275 280 285  
 35 Gly Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln  
 290 295 300  
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 305 310 312

40

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15  
 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30  
 55 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln  
 35 40 45  
 Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
 50 55 60  
 Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp  
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Ile  
80 85 90

5 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly  
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
110 115 120

10 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
125 130 135

Ala Arg Asp Arg Gly Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly  
140 145 150

15 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
155 160 165

20 Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro  
170 175 180

Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr  
185 190 195

25 Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr  
200 205 210

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp  
215 220 225

30 Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg  
230 235 240

Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
245 250 255

35 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg  
260 265 270

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40 Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala  
275 280 285

Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu  
290 295 300

45 Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
305 310

## (2) INFORMATION FOR SEQ ID NO:12:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
-55 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60

AGCGGATAAC AATTCACAC AGG 23

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGAGGGTAG T 21

10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20 Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu  
1 5 10 12

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